SEQUENCE LISTING

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<120> METHODS AND REAGENTS FOR INCREASING PROLIFERATIVE CAPACITY AND PREVENTING REPLICATIVE SENESCENCE

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Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
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cag ggc tgg cgg ctg gtg cag cgc ggg gac ccg gcg gct ttc cgc gcg 203
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala
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Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro
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gcc cga gtg ctg cag agg ctg tgc gag cgc ggc gcg aag aac gtg ctg   347
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu
             85                  90                  95

gcc ttc ggc ttc gcg ctg ctg gac ggg gcc cgc ggg ggc ccc ccc gag   395
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu
        100                 105                 110

gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc gac   443
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp
    115                 120                 125

gca ctg cgg ggg agc ggg gcg tgg ggg ctg ctg ttg cgc cgc gtg ggc   491
Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly
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gac gac gtg ctg gtt cac ctg ctg gca cgc tgc gcg ctc ttt gtg ctg   539
Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu
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gtg gct ccc agc tgc gcc tac cag gtg tgc ggg ccg ccg ctg tac cag   587
Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln
            165                 170                 175

ctc ggc gct gcc act cag gcc cgg ccc ccg cca cac gct agt gga ccc   635
Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro
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cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg gag   683
Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu
    195                 200                 205

gcc ggg gtc ccc ctg ggc ctg cca gcc ccg ggt gcg agg agg cgc ggg   731
Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly
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Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly
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gct gcc cct gag ccg gag cgg acg ccc gtt ggg cag ggg tcc tgg gcc   827
Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala
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cac ccg ggc agg acg cgt gga ccg agt gac cgt ggt ttc tgt gtg gtg   875
His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val
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tca cct gcc aga ccc gcc gaa gaa gcc acc tct ttg gag ggt gcg ctc   923
Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu
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Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala
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ccc ccg gtg tac gcc gag acc aag cac ttc ctc tac tcc tca ggc gac   1067
Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp
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aag gag cag ctg cgg ccc tcc ttc cta ctc agc tct ctg agg ccc agc   1115
Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser
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ccc tgg atg cca ggg act ccc cgc agg ttg ccc cgc ctg ccc cag cgc   1211
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tac tgg caa atg cgg ccc ctg ttt ctg gag ctg ctt ggg aac cac gcg   1259
Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala
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Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala
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gcg gtc acc cca gca gcc ggt gtc tgt gcc cgg gag aag ccc cag ggc   1355
Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly
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tct gtg gcg gcc ccc gag gag gag gac aca gac ccc cgt cgc ctg gtg   1403
Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val
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cag ctg ctc cgc cag cac agc agc ccc tgg cag gtg tac ggc ttc gtg   1451
Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
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cgg gcc tgc ctg cgc cgg ctg gtg ccc cca ggc ctc tgg ggc tcc agg   1499
Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
                470                 475                 480

cac aac gaa cgc cgc ttc ctc agg aac acc aag aag ttc atc tcc ctg   1547
His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
            485                 490                 495

ggg aag cat gcc aag ctc tcg ctg cag gag ctg acg tgg aag atg agc   1595
Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
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cac tgg ctg atg agt gtg tac gtc gtc gag ctg ctc agg tct ttc ttt   1739
His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
                550                 555                 560

tat gtc acg gag acc acg ttt caa aag aac agg ctc ttt ttc tac cgg   1787
Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
            565                 570                 575

aag agt gtc tgg agc aag ttg caa agc att gga atc aga cag cac ttg   1835
Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
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aag agg gtg cag ctg cgg gag ctg tcg gaa gca gag gtc agg cag cat   1883
Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
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cgg gaa gcc agg ccc gcc ctg ctg acg tcc aga ctc cgc ttc atc ccc   1931
Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
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aag cct gac ggg ctg cgg ccg att gtg aac atg gac tac gtc gtg gga   1979
Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
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gcc aga acg ttc cgc aga gaa aag agg gcc gag cgt ctc acc tcg agg   2027
Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
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gtg aag gca ctg ttc agc gtg ctc aac tac gag cgg gcg cgg cgc ccc   2075
Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
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Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
    675                 680                 685

tgg cgc acc ttc gtg ctg cgt gtg cgg gcc cag gac ccg ccg cct gag   2171
Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
690                 695                 700                 705

ctg tac ttt gtc aag gtg gat gtg acg ggc gcg tac gac acc atc ccc   2219
Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
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cag gac agg ctc acg gag gtc atc gcc agc atc atc aaa ccc cag aac   2267
Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
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acg tac tgc gtg cgt cgg tat gcc gtg gtc cag aag gcc gcc cat ggg   2315
Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
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cag ccg tac atg cga cag ttc gtg gct cac ctg cag gag acc agc ccg   2411
Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro
770                 775                 780                 785

ctg agg gat gcc gtc gtc atc gag cag agc tcc tcc ctg aat gag gcc   2459
Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
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agc agt ggc ctc ttc gac gtc ttc cta cgc ttc atg tgc cac cac gcc   2507
Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
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gtg cgc atc agg ggc aag tcc tac gtc cag tgc cag ggg atc ccg cag   2555
Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
        820                 825                 830

ggc tcc atc ctc tcc acg ctg ctc tgc agc ctg tgc tac ggc gac atg   2603
Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
    835                 840                 845

gag aac aag ctg ttt gcg ggg att cgg cgg gac ggg ctg ctc ctg cgt   2651
Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
850                 855                 860                 865

ttg gtg gat gat ttc ttg ttg gtg aca cct cac ctc acc cac gcg aaa   2699
Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
                870                 875                 880

acc ttc ctc agg acc ctg gtc cga ggt gtc cct gag tat ggc tgc gtg   2747
Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
            885                 890                 895

gtg aac ttg cgg aag aca gtg gtg aac ttc cct gta gaa gac gag gcc   2795
Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
        900                 905                 910

ctg ggt ggc acg gct ttt gtt cag atg ccg gcc cac ggc cta ttc ccc   2843
Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
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tgg tgc ggc ctg ctg ctg gat acc cgg acc ctg gag gtg cag agc gac   2891
Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
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tac tcc agc tat gcc cgg acc tcc atc aga gcc agt ctc acc ttc aac   2939
Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
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cgc ggc ttc aag gct ggg agg aac atg cgt cgc aaa ctc ttt ggg gtc   2987
Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
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        980                 985                 990

ctc cag acg gtg tgc acc aac atc tac aag atc ctc ctg ctg cag gcg   3083
Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
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tac agg ttt cac gca tgt gtg ctg cag ctc cca ttt cat cag caa gtt   3131
Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
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tgg aag aac ccc aca ttt ttc ctg cgc gtc atc tct gac acg gcc tcc   3179
Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser
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ctc tgc tac tcc atc ctg aaa gcc aag aac gca ggg atg tcg ctg ggg   3227
Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly
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gcc aag ggc gcc gcc ggc cct ctg ccc tcc gag gcc gtg cag tgg ctg   3275
Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu
       1060                1065                1070

tgc cac caa gca ttc ctg ctc aag ctg act cga cac cgt gtc acc tac   3323
Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr
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gtg cca ctc ctg ggg tca ctc agg aca gcc cag acg cag ctg agt cgg   3371
Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
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aag ctc ccg ggg acg acg ctg act gcc ctg gag gcc gca gcc aac ccg   3419
Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro
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Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
           1125                1130

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         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65                  70                  75                  80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
                 85                  90                  95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
            100                 105                 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
        115                 120                 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
    130                 135                 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145                 150                 155                 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
                165                 170                 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
            180                 185                 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
        195                 200                 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
    210                 215                 220

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Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
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Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
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Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
        275                 280                 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
    290                 295                 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
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Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
                325                 330                 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
            340                 345                 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
        355                 360                 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
    370                 375                 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
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Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
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Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
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Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
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Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
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Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
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Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
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Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
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Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
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Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
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Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
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Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
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Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
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Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
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Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
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Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
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Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
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Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
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Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
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Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
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Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
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Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp
 65                  70                  75                  80

Leu Leu Gly Asp Leu Phe Gly Val Pro Ser Phe Ser Val Lys Glu His
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Arg Lys Ile Tyr Thr Met Ile Tyr Arg Asn Leu Val Val Val Asn Gln
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Gln Glu Ser Ser Asp Ser Gly Thr Ser Val Ser Glu Asn Arg Cys His
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Glu Lys Pro Ser Ser Ser His Leu Val Ser Arg Pro Ser Thr Ser Ser
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Arg Arg Arg Ala Ile Ser Glu Thr Glu Glu Asn Ser Asp Glu Leu Ser
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Gly Glu Arg Gln Arg Lys Arg His Lys Ser Asp Ser Ile Ser Leu Ser
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Phe Asp Glu Ser Leu Ala Leu Cys Val Ile Arg Glu Ile Cys Cys Glu
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Arg Ser Ser Ser Ser Glu Ser Thr Gly Thr Pro Ser Asn Pro Asp Leu
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Asp Ala Gly Val Ser Glu His Ser Gly Asp Trp Leu Asp Gln Asp Ser
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Val Ser Asp Gln Phe Ser Val Glu Phe Glu Val Glu Ser Leu Asp Ser
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Glu Asp Tyr Ser Leu Ser Glu Glu Gly Gln Glu Leu Ser Asp Glu Asp
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Asp Glu Val Tyr Gln Val Thr Val Tyr Gln Ala Gly Glu Ser Asp Thr
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Asp Ser Phe Glu Glu Asp Pro Glu Ile Ser Leu Ala Asp Tyr Trp Lys
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Cys Thr Ser Cys Asn Glu Met Asn Pro Pro Leu Pro Ser His Cys Asn
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Arg Cys Trp Ala Leu Arg Glu Asn Trp Leu Pro Glu Asp Lys Gly Lys
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Glu Glu Thr Gln Asp Lys Glu Glu Ser Val Glu Ser Ser Leu Pro Leu
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Cys Ile Val His Gly Lys Thr Gly His Leu Met Ala Cys Phe Thr Cys
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Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
         35                  40                  45

Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
     50                  55                  60

Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
 65                  70                  75                  80

Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
                 85                  90                  95

Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
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Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
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Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
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Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
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Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
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Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
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Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
        195                 200                 205

Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
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Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg
225                 230                 235                 240

Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro
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Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
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Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
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<212> PRT
<213> Homo sapiens

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Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn His Gln His
         35                  40                  45

Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met Leu Cys Met
     50                  55                  60

Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu Ser Ser Ala
 65                  70                  75                  80

Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr Leu Ser Phe
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Val Cys Pro Trp Cys Ala Ser Gln Gln
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gccgatccag gtcatgatga tgggcagcgc ccgagtggcg gagctgctgc tgctccacgg 240
cgcggagccc aactgcgccg accccgccac tctcacccga cccgtgcacg acgctgcccg 300
ggagggcttc ctggacacgc tggtggtgct gcaccgggcc ggggcgcggc tggacgtgcg 360
cgatgcctgg ggccgtctgc ccgtggacct ggctgaggag ctgggccatc gcgatgtcgc 420
acggtacctg cgcgcggctg cgggggcac cagaggcagt aaccatgccc gcatagatgc 480
cgcggaaggt ccctcagaca tccccgattg aaagaaccag agaggctctg agaaacctcg 540
ggaaacttag atcatcagtc accgaaggtc ctacagggcc acaactgccc ccgccacaac 600
ccaccccgct ttcgtagttt tcatttagaa aatagagctt ttaaaaatgt cctgcctttt 660
aacgtagata taagccttcc cccactaccg taaatgtcca tttatatcat tttttatata 720
ttcttataaa aatgtaaaaa agaaaaacac cgcttctgcc ttttcactgt gttggagttt 780
tctggagtga gcactcacgc cctaagcgca cattcatgtg ggcatttctt gcgagcctcg 840
cagcctccgg aagctgtcga cttcatgaca agcattttgt gaactaggga agctcagggg 900
ggttactggc ttctcttgag tcacactgct agcaaatggc agaaccaaag ctcaaataaa 960
aataaaataa ttttcattca ttcactc 987

<210> 10
<211> 1181
<212> DNA
<213> Homo sapiens

<400> 10
atggaggagc cgcagtcaga tcctagcgtc gagccccctc tgagtcagga aacattttca 60
gacctatgga aactacttcc tgaaaacaac gttctgtccc ccttgccgtc ccaagcaatg 120
gatgatttga tgctgtcccc ggacgatatt gaacaatggt tcactgaaga cccaggtcca 180
gatgaagctc ccagaatgcc agaggctgct ccccccgtgg cccctgcacc agcagctcct 240
acaccggcgg cccctgcacc agccccctcc tggcccctgt catcttctgt cccttcccag 300
aaaacctacc agggcagcta cggtttccgt ctgggcttct tgcattctgg gacagccaag 360
tctgtgactt gcacgtactc ccctgccctc aacaagatgt tttgccaact ggccaagacc 420
tgccctgtgc agctgtgggt tgattccaca cccccgcccg gcacccgcgt ccgcgccatg 480
gccatctaca agcagtcaca gcacatgacg gaggttgtga ggcgctgccc ccaccatgag 540
cgctgctcag atagcgatgg tctggccccc cctcagcatc ttatccgagt ggaaggaaat 600
ttgcgtgtgg agtatttgga tgacagaaac acttttcgac atagtgtggt ggtgccctat 660
gagccgcctg aggttggctc tgactgtacc accatccact acaactacat gtgtaacagt 720
tcctgcatgg gcggcatgaa ccggaggccc atcctcacca tcatcacact ggaagactcc 780
agtggtaatc tactgggacg gaacagcttt gaggtgcgtg tttgtgcctg tcctgggaga 840
gaccggcgca cagaggaaga gaatctccgc aagaaagggg agcctcacca cgagctgccc 900
ccagggagca ctaagcgagc actgcccaac aacaccagct cctctcccca gccaaagaag 960
aaaccactgg atggagaata tttcaccctt cagatccgtg ggcgtgagcg cttcgagatg 1020

ttccgagagc tgaatgaggc cttggaactc aaggatgccc aggctgggaa ggagccaggg 1080
gggagcaggg ctcactccag ccacctgaag tccaaaaagg gtcagtctac ctcccgccat 1140
aaaaaactca tgttcaagac agaagggcct gactcagact g 1181

<210> 11
<211> 540
<212> DNA
<213> Homo sapiens

<400> 11
cgcgcctgcg gggcggagat gggcaggggg cggtgcgtgg gtcccagtct gcagttaagg 60
gggcaggagt ggcgctgctc acctctggtg ccaaagggcg gcgcagcggc tgccgagctc 120
ggccctggag gcggcgagaa catggtgcgc aggttcttgg tgaccctccg gattcggcgc 180
gcgtgcggcc cgccgcgagt gagggttttc gtggttcaca tcccgcggct cacgggggag 240
tgggcagcgc caggggcgcc cgccgctgtg gccctcgtgc tgatgctact gaggagccag 300
cgtctagggc agcagccgct tcctagaaga ccaggtcatg atgatgggca gcgcccgagt 360
ggcggagctg ctgctgctcc acggcgcgga gcccaactgc gccgaccccg ccactctcac 420
ccgacccgtg cacgacgctg cccgggaggg cttcctggac acgctggtgg tgctgcaccg 480
ggccggggcg cggctggacg tgcgcgatgc ctggggccgt ctgcccgtgg acctggctga 540

<210> 12
<211> 26
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: internalizing
peptide

<400> 12
Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
1 5 10 15

Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser
20 25

<210> 13
<211> 12
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: EGF derived
peptide

<400> 13
Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys
1 5 10

<210> 14
<211> 12
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: EGF derived
peptide

<400> 14
Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
1 5 10

<210> 15
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: internalizing
peptide

<220>
<221> MOD_RES
<222> (1)
<223> unique residue, such as cysteine or lysine, that
facilitates chemical conjugation of the
internalizing peptide to a target protein
conjugate.

<220>
<221> MOD_RES
<222> (2)..(3)
<223> amino acid residue selected to modulate the
affinity of the internalizing peptide for
different membranes.

<400> 15
Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala
1 5 10 15

Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
20 25 30

<210> 16
<211> 8
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: peptide substrate

<400> 16
Gly Asn Ala Ala Ala Ala Arg Arg
1 5

<210> 17
<211> 10
<212> PRT

<213> Unknown Organism

<220>
<223> Description of Unknown Organism: laminin derived
peptide

<400> 17
Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys
1 5 10

<210> 18
<211> 75
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Nde1-EcoR1
fragment

<400> 18
catatgggtg gctgccgtgg cgatatgttc ggttgcggtg ctcctccaaa aaagaagaga 60
aaggtagctg gattc 75

<210> 19
<211> 24
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: RGD/SV40 peptide

<400> 19
Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys
1 5 10 15

Lys Lys Arg Lys Val Ala Gly Phe
20

<210> 20
<211> 225
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Nde1-EcoR1
fragment

<400> 20
catatggagc cagtagatcc tagactagag ccctggaagc atccaggaag tcagcctaaa 60
actgcttgta ccaattgcta ttgtaaaaag tgttgctttc attgccaagt ttgtttcata 120
acaaaagccc ttggcatctc ctatggcagg aagaagcgga gacagcgacg aagacctcct 180
caaggcagtc agactcatca agtttctcta agtaagcaag gattc 225

<210> 21
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: engineered HIV-1 tat

<400> 21
Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
50 55 60

His Gln Val Ser Leu Ser Lys Gln
65 70

<210> 22
<211> 912
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Nde1-EcoR1
fragment

<400> 22
catatgacct ctcgccgctc cgtgaagtcg ggtccgcggg aggttccgcg cgatgagtac 60
gaggatctgt actacacccc gtcttcaggt atggcgagtc ccgatagtcc gcctgacacc 120
tcccgccgtg gcgccctaca gacacgctcg cgccagaggg gcgaggtccg tttcgtccag 180
tacgacgagt cggattatgc cctctacggg ggctcgtcat ccgaagacga cgaacacccg 240
gaggtccccc ggacgcggcg tcccgtttcc ggggcggttt tgtccggccc ggggcctgcg 300
cgggcgcctc cgccacccgc tgggtccgga ggggccggac gcacacccac caccgccccc 360
cgggcccccc gaacccagcg ggtggcgact aaggcccccg cggccccggc ggcggagacc 420
acccgcggca ggaaatcggc ccagccagaa tccgccgcac tcccagacgc ccccgcgtcg 480
acggcgccaa cccgatccaa gacacccgcg caggggctgg ccagaaagct gcactttagc 540
accgcccccc caaaccccga cgcgccatgg acccccgggg tggccggctt taacaagcgc 600
gtcttctgcg ccgcggtcgg gcgcctggcg gccatgcatg cccggatggc ggcggtccag 660
ctctgggaca tgtcgcgtcc gcgcacagac gaagacctca acgaactcct tggcatcacc 720
accatccgcg tgacggtctg cgagggcaaa aacctgcttc agcgcgccaa cgagttggtg 780
aatccagacg tggtgcagga cgtcgacgcg gccacggcga ctcgagggcg ttctgcggcg 840
tcgcgcccca ccgagcgacc tcgagcccca gcccgctccg cttctcgccc cagacggccc 900
gtcgaggaat tc 912

<210> 23
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: engineered HSV-1 VP22

<400> 23
Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro Arg
1 5 10 15

Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser
20 25 30

Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg
35 40 45

Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp
50 55 60

Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu
65 70 75 80

Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro
85 90 95

Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly
100 105 110

Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gly Arg Val Ala
115 120 125

Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys
130 135 140

Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr
145 150 155 160

Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu
165 170 175

His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg
180 185 190

Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu
195 200 205

Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser
210 215 220

Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr
225 230 235 240

Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn
245 250 255

Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala
260 265 270

Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala

275 280 285

Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu
290 295 300

<210> 24
<211> 120
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Nde1-EcoR1
fragment

<400> 24
catatggacg tcgacgcggc cacggcgact cgagggcgtt ctgcggcgtc gcgccccacc 60
gagcgacctc gagccccagc ccgctccgct tctcgcccca gacggcccgt cgaggaattc 120

<210> 25
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: VP22 (C-terminal domain)

<400> 25
Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser
1 5 10 15

Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro
20 25 30

Arg Arg Pro Val Glu
35

<210> 26
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative
peptide

<400> 26
Cys Ala Ala Met
1

<210> 27
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative
peptide

<400> 27
Cys Ala Ala Ser
1

<210> 28
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 28
aatccgtcga gcagagtt 18

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
gcgcggctaa ccctaaccct aacc 24

<210> 30
<211> 1031
<212> PRT
<213> Euplotes sp.

<400> 30
Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
1 5 10 15

Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
20 25 30

Asn Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
35 40 45

Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
50 55 60

Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
65 70 75 80

Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
85 90 95

```
Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
            100                 105                 110

Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
        115                 120                 125

Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
    130                 135                 140

Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
145                 150                 155                 160

Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
                165                 170                 175

Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
            180                 185                 190

Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
        195                 200                 205

Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
    210                 215                 220

Asn Asn Ile Asn Val Pro Asn Asn Asn Asn Met Lys Ser Arg Thr Arg
225                 230                 235                 240

Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
                245                 250                 255

His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
            260                 265                 270

Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
        275                 280                 285

Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
    290                 295                 300

Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
305                 310                 315                 320

Glu Asn Asn Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
                325                 330                 335

Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
            340                 345                 350

Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
        355                 360                 365

Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
    370                 375                 380

Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
385                 390                 395                 400
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Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
405 410 415

Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
420 425 430

Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
435 440 445

Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
450 455 460

Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
465 470 475 480

Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
485 490 495

Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
500 505 510

Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
515 520 525

Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
530 535 540

Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
545 550 555 560

Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
565 570 575

Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
580 585 590

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
595 600 605

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
610 615 620

Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
625 630 635 640

Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
645 650 655

Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
660 665 670

Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
675 680 685

Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
690 695 700

Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
705 710 715 720

Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
725 730 735

Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
740 745 750

Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
755 760 765

Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
770 775 780

Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
785 790 795 800

Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
805 810 815

Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
820 825 830

Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile
835 840 845

Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn
850 855 860

Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr
865 870 875 880

Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met
885 890 895

Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe
900 905 910

Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr
915 920 925

Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala
930 935 940

Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
945 950 955 960

Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
965 970 975

Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
980 985 990

Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
995 1000 1005

```
Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln
   1010                1015                1020

Ser Leu Ile Gln Tyr Asp Ala
1025                1030


<210> 31
<211> 884
<212> PRT
<213> Saccharomyces cerevisiae

<400> 31
Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
  1               5                  10                  15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn
             20                  25                  30

Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
         35                  40                  45

Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
     50                  55                  60

Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
 65                  70                  75                  80

Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
                 85                  90                  95

Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
            100                 105                 110

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
        115                 120                 125

Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
    130                 135                 140

Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
145                 150                 155                 160

Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
                165                 170                 175

Trp Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
            180                 185                 190

Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
        195                 200                 205

Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
    210                 215                 220

Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
```

225 230 235 240

Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
245 250 255

Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
260 265 270

His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
275 280 285

Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
290 295 300

Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu Pro
305 310 315 320

Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu
325 330 335

Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
340 345 350

Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
355 360 365

Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr
370 375 380

Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp
385 390 395 400

Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu
405 410 415

Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn
420 425 430

Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu
435 440 445

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
450 455 460

Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
465 470 475 480

Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
485 490 495

Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
500 505 510

Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
515 520 525

Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met

530 535 540

Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
545 550 555 560

Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
565 570 575

Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
580 585 590

Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
595 600 605

Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
610 615 620

Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
625 630 635 640

Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
645 650 655

Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
660 665 670

Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
675 680 685

Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
690 695 700

Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
705 710 715 720

Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
725 730 735

Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
740 745 750

Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
755 760 765

Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
770 775 780

His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
785 790 795 800

Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
805 810 815

Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
820 825 830

Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu

835 840 845

Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
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Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
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His Ile Val Asn

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